PRINTER RUSH (PTO ASSISTANCE)

| Application : | 09/721,4- | Examiner: | J. CHEN | GAU: | 1648 | |
|---|-------------------|--------------|--------------|------------|----------|--|
| From: | R. MITCH | EU Location: | (DC) FMF FDC | Date: | 10/20/05 | |
| Tracking #: <u>EPM 09/721, 47</u> 9 Week Date: <u>5/9/05</u> | | | | | | |
| ı | | | | | | |
| | DOC CODE | DOC DATE | MISCELL | ANEOUS | | |
| | □ 1449 | | _ Continuing | Data | | |
| | ☐ IDS | | Foreign Pri | ority | | |
| | CLM | | _ Document I | Legibility | | |
| | | | Fees | | | |
| | ∏ SRFW ☑ DRW | 4/21/04 | Other | | | |
| | OATH | 110101 | - | | | |
| | 312 | | - | | | |
| | SPEC | | - | | | |
| | | | | | | |
| [RUSH] MESSAGE: ATTENTION CHIEF DRAFTS PERSON | | | | | | |
| FIGS. 11C, 11F, 11G, 14D, 14E, 14G, 14H, 17C, 18B, 18E, 21I, 22E HAS DATE STAMP OVER DATA. | | | | | | |
| - ITHE STATE OVER DATA | | | | | | |
| THANK YOU | | | | | | |
| Kem | | | | | | |
| CYPLICIT DECDONCE. | | | | | | |
| [XRUSH] RESPONSE: — SEE ATTACHMENTS | | | | | | |
| | | | | | | |
| - DRAWINGS CORRECTED | | | | | | |
| INITERIAL C. OZ | | | | | | |
| NOTE: This form will be included as part of the official USPTO record, with the Response | | | | | | |

document coded as XRUSH. REV 10/04

- 662 TGCAATACGTGTGACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAG ACGTTATGCACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTC
- ThrileThrLeuProGlnAspAleValSerArgThrGlnArgArgGlyArgThrGlyArg
 ACAATCACGCTCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGG
 TGTTAGTGCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCC
- GlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAsp GGGAAGCCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGAC CCCTTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTG

822 BGLI, 839 DRD1,

887 SACI,

GluThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAsp 902 GAGACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGAC CTCTGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTG

937 SMAI XMAI,

991 STUI,

1075 DRA3,

- SerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrVal
 1022 TCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTG
 AGGGTCTGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCAC
- CysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArg
 1082 TGCGCTAGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGC
 ACGCGATCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACAAACTAAGCG
- LeulysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsn
 1142 CTCAAGCCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAAT
 GAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTA
 1156 NCOI.
- - 1236 BSPH1, 1240 DRD1, 1243 AVA3, 1251 EAG1 XMA3, 1256 DRD1,
- GluValValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyr GAGGTCGTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCTTGGCCGCGTAT CTCCAGCAGTGCTCGTGGACCCACGAGCAACCGCCGAGAACCGGCGCATA

CysleuSerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAla 1322 TGCCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCA ACGGACAGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGT

1375 NAEI.

IleIleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGln ATCATACCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAG TAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACCTTCTCACGAGAGTC

1391 DRD1,

- HisLeuProTyrlleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeu
 1442 CACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTC
 GTGAATGGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAG
- GlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsn GGCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAAC CCGGAGGACGTCTGGCGCAGGCCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTG

1508 PSTI, 1513 TTH31,

TrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGln
1562 TGGCAAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAA
ACCGTTTTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTT

1571 XHOI, 1592 NDEI,

TyrleuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPhe 1622 TACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTT ATGAACCGCCCGAACAGTTGCGACGACCATTGGGGCGGTAACGAAGTAACTACCGAAAA

1649 BSTE2,

ThiAlaAlaValThiSerPioLeuThiThiSerGlnThiLeuLeuPheAsnileLeuGly
1682 ACAGCTGCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGG
TGTCGACGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAGTTGTATAACCCC

1683 ALWN1 PVU2,

GlyTrpValAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGly
1742 GGGTGGGTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGC
CCCACCCACCGACGGTCGAGCGGGGGCCACGGCGATGACGGAAACACCCGCGACCG

1800 ESP1,

LeuAlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAla
1802 TTAGCTGGCGCCCCATCGGCAGTGTTGGACTGGGAAGGTCCTCATAGACATCCTTGCA
AATCGACCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGT

1808 KAS1 NARI,

GlyTyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluVal 1862 GGGTATGGCGGGGGGGGGGGGGGGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTC CCCATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAG

- IleLeuArgLysSerArgArgPheAleGlnAleL uProVelTrpAleArgPr AspTyr ATCCTGCGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTAT TAGGACGCCTTCAGAGCCTCTAAGCGGGTCCGGACGGCCAAACCCGCGCCGGCCTGATA
 - 3149 ALWN1, 3170 EAG1 KMA3,
- AsnProProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGly
 3182 AACCCCCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGACCACCTGTGGTCCATGGC
 TTGGGGGGGGGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCG
 - 3223 HGIE2, 3235 NCOI,
- CysProLeuProProProLysSerProProValProProProArgLysLysArgThrVal
 3242 TGCCCGCTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTG
 ACGGGCGAAGGTGGAGGTTTCAGGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCAC
- ValLeuThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGly
 3302 GTCCTCACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGC
 CAGGAGTGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCG
 - 3338 SACI, 3352 HIND3,
- SerGlyCysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGly
 3422 TCTGGCTGCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGG
 AGACCGACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCC
 - 3443 EAM11051,
- GluProGlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsn
 3482 GAGCCTGGGGATCCTGGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTGAGGCCAAC
 CTCGGACCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTG
 - 3490 BAMHI, 3491 BSAB1, 3493 BSPE1,
- AlaGluAspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrPro 3542 GCGGAGGATGTCGTGTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCG CGCCTCCTACAGCACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGC
 - 3595 DRA3,
- CysAlaAlaGluGluLysLeuProlleAsnAlaLeuSerAsnSerLeuLeuArgHis TGCGCCGCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCAC ACGCGGCGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTG
 - 3606 SAC2, 3617 ALWN1, 3661 PFLM1.
- HisAsnleuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThr
 3662 CACAATTTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACA
 GTGTTAAACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGT
 - 3687 DRA3,
 - PheAspArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAla

- TTTGACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCA AAACTGTCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGT AlaAlaSerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrPro GCGGCGTCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCC 3782 CGCCGCAGTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGG 3822 HIND3. ProHisSerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArg CCACACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGA GGTGTGAGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCT 3881 AAT2, 3896 BGLI, LysAlaValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrPro AAGGCCGTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCA TTCCGGCATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGT ${\tt IleAspThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGly}$ 3962 ATAGACACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGGT TATCTGTGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCA ArgLysProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMet CGTAAGCCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATG GCATTCGGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTAC AlaLeuTyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPhe GCTTTGTACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTC CGAAACATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAG GlnTyrSerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThr CAATACTCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACC GTTATGAGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGG 4166 ECORI, ProMetGlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIle 4202 CCAATGGGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATC **GGTTACCCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAG** 4235 DRD1, 4242 ALWN1, ArgThrGluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIle CGTACGGAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATC GCATGCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAG 4307 BGLI, 4314 BALI,
- LysSerLeuThrGluArqLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsn
 4322 AAGTCCCTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAAC
 TTCAGGGAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTG
 4351 APAI,
- CysGlyTyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeu 4382 TGCGGCTATCGCAGGTGCCGCGCGGGGGGGGGGGGGAACTAGCTGTGGTAACACCCTC

- ThrGluAspLeuValAsnLeuLeuProAlaIl LeuSerProGlyAlaLeuValValGly
 1922 ACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGC
 TGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAGCCG
 1928 TH31,
- ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp GTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGGAGTGCAGTGG CACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCCGTCACGTCACC

2004 NAEI, 2017 SMAI XMAI,

- MetAsnArgLeulleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal
 ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTACGTG
 TACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGCGTGATGCAC
 - 2067 SMAI XMAI, 2093 DRA3,
- ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln
 CCGGAGAGCGATGCAGCTGCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAG
 GGCCTCTCGCTACGTCGACGGGCGCAGTGACGTATGAGTCGTCGGAGTGACATTGGGTC
 - 2115 PVU2, 2159 ALWN1,
- LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer CTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCC GAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCAAGG
 - 2164 MST2, 2220 ECON1,
- TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu
 2222 TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTA
 ACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGACCGAT
- LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle
 2342 AAGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAGATC
 TTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG
- ThrGlyHisValLysAsnGlyThrMetArglleValGlyProArgThrCysArgAsnMet
 2402 ACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAACATG
 TGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTTGTAC
 - 2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI,
- TrpSerGlyThrPheProlleAsnAlaTyrThrThrGlyProCysThrProLeuProAla 2462 TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCCTGCG ACCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGACGC
 - 2480 ASE1, 2497 APAI,
 - ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln

- 2522 CCGAACTACACGTTCGCGCTATGGAGGGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAGGGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
- ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln
 2582 GTGGGGGACTTCCACTACGTGACGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG
 CACCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC

2594 DRA3,

- ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro GTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC CAGGGTAGCGGGGTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG
- ProCyslysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro
 CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCG
 GGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC

2757 HGIE2,

ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
2762 GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTC
CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG

2809 AAT2,

ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
2022 ACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCC
TGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCTAGTGGG

2850 EAG1 XMA3,

ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys
CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG

2889 BALI, 2903 NHEI,

ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
ACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAG
TGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC

2966 ESP1, 2969 SACI,

- GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer 3002 GAGATGGGCGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG
- PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu
 TTCGATCCGCTTGTGGCGGAGGAGGAGGACGAGGAGATCTCCGTACCCGCAGAAATCCTG
 AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC

3096 BGL2.

ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro
3122 CGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCC

| 3782 | SerLysVallysAlaAsnLeuLeuSerValGluGluAlaCysS rLeuThrProProHis TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCACAC AGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG |
|------|---|
| | 3816 HIND3, |
| 3842 | SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAGGCC AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG |
| | 3875 AAT2, 3890 BGLI, |
| 3902 | ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp GTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAATAGAC CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG |
| 3962 | ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGGTCGTAAG TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGCATTC |
| 4022 | ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu CCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGCTTTG GGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGAAAC |
| 4082 | TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATAC ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATG |
| 4142 | SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet TCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGTTAC |
| | 4160 ECORI, |
| 4202 | GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG CCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGC |
| | 4229 DRD1, 4236 ALWN1, |
| 4262 | GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCC CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGGTTCGGGCGCACCGGTAGTTCAGG |
| | 4301 BGLI, 4308 BALI, |
| 4322 | LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGlyCTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGCGAGATGGCTCCCCCCTCTTGACGCCGGAGATGGTTAAGTTCCCCCCCTCTTGACGCCG |
| | 4345 APAI, |
| 4382 | TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys TATCGCAGGTGCCGCGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTCACTTGC |

ATAGCGTCCACGGCGCGCCCCCCATGACTGTTGATCGACACCATTGTGGGAGTGAACG

TyrilelysklakrgklaklaCyskrgklaklaGlyLeuGlnAspCysThrMetLeuVal TACATCAAGGCCCGGGCAGCCTGTCGAGCCCAGGGCTCCAGGACTGCACCATGCTCGTG ATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGCTACGAGCAC

6652 SMAI KMAI,

CysGlyAspAspLeuValVallleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
4502 TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGGGGAGC
ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCCAGGTCCTCCTGCGCCCCCCG

4508 DRD1, 4511 TTH31.

- LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
 4562 CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCTGGGGACCCCCCACAA
 GACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGACCCCTGGGGGGTGTT
- ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
 4622 CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC
 GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTG

4637 SACI,

GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla
4682 GGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCCTACAACCCCCCTCGCGAGAGCT
CCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGGAGCGCTCTCGA

4731 NRUI,

- AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe GCGTGGGAGACAGCAAGACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT CGCACCCTCTGTCGTTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA
- AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla GCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC CGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG

4806 PFLM1, 4807 DRA3,

ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu 4862 AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAA TCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT

4893 BGL2,

ProLeuAspleuProProlleTleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis 4922 CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG

4954 NCOI.

SerTyrSerProGlyGlulleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro 4982 AGTTACTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC

5015 SPHI, 5035 KPNI,

ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly

TCCCGAGTTCGGGGAGGGGGTAGCACCTTGGTCTACACCTTCACAAACTAAGCGGAGTTC

- ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
 CCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC
 GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG

 1150 NCOI.
- - 1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,
- ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu 1262 GTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTGCCTG CAGTGCTCGTGGACCCACGAGCCACCGCCGCAGAACCGGCGCATAACGGAC
- SerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIle
 1322 TCAACAGGCTGCTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATA
 AGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTAT
 1369 NAEI.
- ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSergInHisLeu
 1382 CCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGAGTGCTCTCAGCACTTA
 GGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACCTTCTCACGAGAGTCGTGAAT
 1385 DRD1.
- ProTyrileGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu 1442 CCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTC GGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAG
- LeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGln
 CTGCAGACCGCGTCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTGGCAA
 GACGTCTGGCGCAGGCCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTT

 1502 PSTI, 1507 TTH31.
- LysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeu
 AAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
 TTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATGAAC
 1565 XHOI, 1586 NDEI.
- AlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAla GCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCT CGCCCGAACAGTTGCGACGGACCATTGGGGCGGTAACGAAGTAACTACCGAAAATGTCGA
 - 1643 BSTE2, 1677 ALWN1 PVU2,
- AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp

 1682 GCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGGGTGG

 CGACAGTGGTCGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCCCACC

- ValalaAlaGlnLeuAlaAlaPr GlyAlaAlaThrAlaPheValGlyAlaGlyLeuAla GTGGCTGCCCAGCTCGCCCCCCGGTGCCGCTACTGCTTTGTGGGCGCTGGCTTAGCT CACCGACGGGTCGAGCGGGGGCCCACGGCGATGACGGAAACACCCGGGACCGAATCGA
- GlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyr GGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGGGTAT CCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCCATA

1802 KAS1 NARI,

1794 ESP1.

GlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSer GGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCCTCC CCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGG

1878 SACI, 1899 BSPH1,

- ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGly
 1922 ACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGC
 TGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAGCCG
 1928 TTH31.
- ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp 1982 GTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGGCAGTGCAGTGG CACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCCGTCACGTCACC

2004 NAEI, 2017 SMAI XMAI,

MetAsnArgLeulleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal
ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTACGTG
TACTTGGCCGACTATCGGAAGCGGAGGCCCCCTTGGTACAAAGGGGGTGCGTGATGCAC

2067 SMAI XMAI, 2093 DRA3,

ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln CCGGAGAGCGATGCAGCTGCCGGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAG GGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTC

2115 PVU2, 2159 ALWN1,

LeuleuArgArgleuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer
CTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCC
GAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCAAGG

2164 MST2, 2220 ECON1,

- TrpleuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu
 TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTA
 ACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGACCGAT

2285 ESP1, 2300 PVU2, 2310 BAMHI,

FIG. 17D

- ThrCysValThrGlnThrValAspPheSerLeuAspPr ThrPheThrIleGluThrIle ACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCCTTCACCATTGAGACAATC TGCACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGAAGTGGTAACTCTGTTAG
- ThrLeuProGlnAspAleValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
 ACGCTCCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAG
 TGCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTC
- ProglylleTyrArgPheValAlaProglyGluArgProSerGlyMetPheAspSerSer
 CCAGGCATCTACAGATTTGTGGCACCGGGGGGGGCGCCCCTCCGGCATGTTCGACTCGTCC
 GGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGG
 - 816 BGLI, 833 DRD1,
- - 881 SACI,
- ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
 902 ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTT
 TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGAA
 - 931 SMAI XMAI,
- GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln 962 GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAG CTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC
 - 985 STUI,
- ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla ACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGA
 - 1069 DRA3,
- ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
 1082 AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAG
 TCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACACTTCACAAACTAAGCGGAGTTC
- ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle CCCACCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG 1150 NCOI.
- - 1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,
- ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu 1262 GTCACGAGCACCTGGGTGCTCGTTGGCCGCGTCCTGGCTGCTTTGGCCGCGTATTGCCTG

- ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln
 CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG
 GGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
 2553 PSTI,
- ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG CACCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC 2594 DRA3.
- ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro GTCCCATCGCCCGAATTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC CAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG
- ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro
 CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCG
 GGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC
 2757 HGIE2.
- ValGlySerGinLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
 2762 GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACCGTGTGACGTCCATGCTC
 CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG
 2809 AAT2.
- ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
 ACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCC
 TGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCTAGTGGG
 2850 EAG1 XMA3.
- ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys
 CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
 GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG
 2889 BALI. 2903 NHEI.
- ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
 ACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAG
 TGGCGATTGGTACTGAGGGGACTACGACTCCGGTTTGGAGGATACCTCCGTC
 2966 ESP1, 2969 SACI.
- GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer 3002 GAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG
- PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu
 TTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGAATCCTG
 AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC
 3096 BGL2.

ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro

- ProleuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
 5042 CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGGCCTAGGCTTCTGGCCAGAGACGGTCCCT
 GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTCTCCT
 - 5064 APAI, 5091 BALI,
- GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys 5102 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA CCGTCCCGACGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT
 - 5113 NDEI,
- - 5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,
- SerglyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys
 AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTGC
 TCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGCGACCTAGACCAAAACG
 - 5240 DRA3,
- LeuleuleuleuAlaAlaGlyValGlyIleTyrLeuleuProAsnArgMetSerThrAsn
 5282 CTACTCCTGCTTGCTGCAGGGGTAGGCATCTCCTCCCCAACCGAATGAGCACGAAT
 GATGAGGACGACGACGTCCCATCCGTAGATGGAGGAGGGGTTGGCTTACTCGTGCTTA
 - 5295 PSTI.
- ProlysproglnArglysThrLysArgAsnThrAsnArgArgProglnAspVallysPhe
 5342 CCTAAACCTCAAAGAAAGACCAAACGTAACACCAACCGGGGGCGCGCAGGACGTCAAGTTC
 GGATTTGGAGTTCTTCTTGGTTTGCATTGTGGTTGGCCGCGGCGTCCTGCAGTTCAAG
 - 5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI,
- ProGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu
 5402 CCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTG
 GGCCCACCGCCAGTCTAGCAACCACCTCAAATGAACAACGGCGCGTCCCCGGGATCTAAC
 - 5.449 APAI,
- GlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro
 5462 GGTGTGCGCGCGACGAGAAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTCAGCCT
 CCACACGCGCGCGCTGCTCTTTCTGAAGGCTCGCCAGCGTTGGAGCTCCATCTGCAGTCGGA
 - 5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,
- IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpPro
 5522 ATCCCCAAGGCTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGCCC
 TAGGGGTTCCGAGCAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGCCCATGGGAACCGGG
 - 5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,
- LeutyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg
 5582 CTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGGCTCTCGG
 GAGATACCGTTACTCCCGACGCCCCACCCGCCCTACCGAGGACAGAGGGGCACCGAGAGCC

4229 DRD1, 4236 ALWN1.

GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer 4262 GAGGAGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCC CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTTCAGG

4301 BGLI, 4308 BALI,

LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
4322 CTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGGAGAACTGCGGC
GAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCCTCTTGACGCCG

4345 APAI,

- TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
 4382 TATCGCAGGTGCCGCGCGCGCGCGTACTGACAACTAGCTGTGGTAACACCCTCACTTGC
 ATAGCGTCCACGGCGCGCTCGCCGCATGACTGTGATCGACACCATTGTGGGAGTGAACG
- TyrilelysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
 TACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTG
 ATGTAGTTCCGGGGCCCGTCGGACAGCTCCGGGGTCCTGACGTGGTACGAGCAC

4452 SMAI XMAI,

- CysGlyAspAspLeuValVallleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
 4502 TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGCGAGC
 ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGCTCG
 4508 DRD1, 4511 TTH31,
- LeuArgalaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
 4562 CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCCTGGGGACCCCCCACAA
 GACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGGACCCCTGGGGGGTGTT
- ProGlutyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
 4622 CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC
 GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTG

4637 SACI,

GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla 4682 GGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCCTACAACCCCCCTCGCGAGAGCT CCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGGAGCGCTCTCGA

4731 NRUI.

- AlatrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe 4742 GCGTGGGAGACAGCAAGACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT CGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA
- AleprothrleutrpaleargmetileLeuMetthrHisPhePheSerValLeuIleale GCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC CGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG

4806 PFLM1, 4807 DRA3,

ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu

- 4862 AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAA
 TCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT

 4893 BGL2.
- ProLeuAspleuProProllelleGlnArgleuHisGlyLeuSerAlaPheSerLeuHis
 4922 CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC
 GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG
 4954 NCOI,
- SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC
 - 5015 SPHI, 5035 KPNI,
- ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
 CCCTTGCGAGCTTGGAGACACCGGGCCCGGGCCTCGCAGGCGTTCTGGCCAGAGGA
 GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTCTCCT
 - 5064 APAI, 5091 BALI,
- GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys
 5102 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA
 CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT
 5113 NDEI.
- - 5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,
- SerGlyGlyAsplleTyrHisSerValSerHisAlaArgProArgTrplleTrpPheCys
 AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTGC
 TCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGCGACCTAGACCAAAACG
 - 5240 DRA3,
- LeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgMetSerThrAsn CTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGAATGAGCACGAAT GATGAGGACGACGACGTCCCCATCCGTAGATGAGGAGGGGGTTGGCTTACTCGTGCTTA \$295 PSTI.
- ProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspValLysPhe
 5342 CCTAAACCTCAAAGAAAGACCAAACGTAACACCAACCGGCGCCGCGGGACGTCAAGTTC
 GGATTTGGAGTTCTTCTGGTTTGCATTGTGGTTGGCCGCCGGCGTCCTGCAGTTCAAG
 - 5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI,

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- LysGlyValTxpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle
 2342 AAGGGGTCTGGCGAGGGGACGCCATCATGCACACTCGCTGCCACTGTGGAGCTCAGATC
 TTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG
- ThrGlyHisVallysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMet
 ACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAACATG
 TGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCCAGGATCCTGGACGTCCTTGTAC
 - 2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI,
- TrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla
 TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCCTGCG
 ACCTCACCCTGGAAGGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGACGC
 - 2480 ASE1, 2497 APAI,
- ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln
 CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG
 GGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
 - 2553 PSTI.
- ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln 2582 GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG CACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC
 - 2594 DRA3.
- ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro GTCCCATCGCCCGAATTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC CAGGGTAGCGGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG
- ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCG GGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC
 - 2757 HGIE2,
- ValGlySerGinLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu 2762 GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTC CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG
 - 2809 AAT2,
- ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
 2822 ACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGCCGAAGGTTGGCGAGGGGATCACCC
 TGACTAGGGAGGGTATATTGTCGTCTCCCCCGGCCCGCTTCCAACCGCTCCCCTAGTGGG
 - 2850 EAG1 XMA3.
- ProserValAlaserSerSerAlaserGlnLeuserAlaProserLeuLysAlaThrCys
 2882 CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
 GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG
 - 2889 BALI, 2903 NHEI,

FIG. 22E